

-continued

---

115	120	125
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu		
130	135	140
Leu Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp		
145	150	155
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Leu Thr Trp Pro Pro Val		
	165	170
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp		
	180	185
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His		
	195	200
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro		
	210	215
Gly Lys		
225		

---

1.-36. (canceled)

**37.** An isolated heteromultimer comprising a modified heterodimeric CH3 domain comprising:

a first CH3 domain polypeptide and a second CH3 domain polypeptide, each independently comprising amino acid modifications as compared to a wild-type CH3 domain polypeptide, wherein the amino acid modifications promote formation of a heterodimeric CH3 domain as compared to a homodimeric CH3 domain; wherein at least one of the first and second CH3 domain polypeptides comprises a T350X modification, wherein X is selected from valine, isoleucine, leucine and methionine;

wherein

the first CH3 domain polypeptide comprises amino acid modifications at positions F405 and Y407, and the second CH3 domain polypeptide comprises an amino acid modification at position T394, wherein the amino acid modification at position F405 is F405A, F405S, F405T or F405V; the amino acid modification at position Y407 is Y407I or Y407V, and the amino acid modification at position T394 is T394W;

wherein the modified heterodimeric CH3 domain is comprised by an Fc construct based on a type G immunoglobulin (IgG), and

wherein the numbering of amino acid residues is according to the EU index as set forth in Kabat.

**38.** Nucleic acid encoding the isolated heteromultimer according to claim **37**.

**39.** A vector comprising the nucleic acid according to claim **38**.

**40.** A mammalian host cell comprising nucleic acid encoding the isolated heteromultimer according to claim **37**.

**41.** A composition comprising the isolated heteromultimer according to claim **37** and a pharmaceutically acceptable carrier.

**42.** (canceled)

**43.** The isolated heteromultimer according to claim **37**, wherein the T350X modification is a T350V modification.

**44.** The isolated heteromultimer according to claim **43**, wherein both the first and second CH3 domain polypeptides comprise a T350V modification.

**45.** The isolated heteromultimer according to claim **37**, wherein the second CH3 domain polypeptide further comprises an amino acid modification at position T366 selected from T366I, T366L, T366M and T366V.

**46.** The isolated heteromultimer according to claim **45**, wherein the amino acid modification at position T366 is T366I or T366L.

**47.** The isolated heteromultimer according to claim **37**, wherein the second CH3 domain polypeptide further comprises an amino acid modification at position K392 selected from K392F, K392L and K392M.

**48.** The isolated heteromultimer according to claim **47**, wherein the amino acid modification at position K392 is K392L or K392M.

**49.** The isolated heteromultimer according to claim **37**, wherein the first CH3 domain polypeptide or the second CH3 domain polypeptide or both the first and second CH3 domain polypeptides further comprises the amino acid modification L351Y.

**50.** The isolated heteromultimer according to claim **37**, wherein the amino acid modification at position F405 is F405A.

**51.** The isolated heteromultimer according to claim **37**, wherein the amino acid modification at position Y407 is Y407V.

**52.** The isolated heteromultimer according to claim **37**, wherein the amino acid modification at position F405 is F405A and the amino acid modification at position Y407 is Y407V.

**53.** The isolated heteromultimer according to claim **52**, wherein the second CH3 domain polypeptide further comprises:

- (a) an amino acid modification at position T366 selected from T366I, T366L, T366M and T366V, or
- (b) an amino acid modification at position K392 selected from K392F, K392L and K392M, or
- (c) an amino acid modification at position T366 selected from T366I, T366L, T366M and T366V, and an amino